

SEQUENCE LISTING

<110> Duprat, Fabrice
Lesage, Florian
Fink, Michel
Lazdunski, Michel

<120> FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING
AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS

<130> 1201-CIP-DIV-2-00

<141> 2001-08-24

<150> 09/144,914
<151> 1998-09-01

<150> 08/749,816
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<150> FR 96/01565
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<170> PatentIn Ver. 2.0

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cg 20 25 30
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 Tyr Glu Asp Leu Leu Arg Gln Glu Leu Arg Lys Leu Lys Arg Arg Phe
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 Leu Glu Glu His Glu Cys Leu Ser Glu Gln Gln Leu Glu Gln Phe Leu
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 Ser Thr Ile Gly Leu Gly Asp Tyr Val Pro Gly Glu Gly Tyr Asn Gln
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 Lys Phe Arg Glu Leu Tyr Lys Ile Gly Ile Thr Cys Tyr Leu Leu Leu
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 Gly Leu Ile Ala Met Leu Val Val Leu Glu Thr Phe Cys Glu Leu His
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 Glu Leu Lys Lys Phe Arg Lys Met Phe Tyr Val Lys Lys Asp Lys Asp
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 Ile Thr Asp Gln Ala Ala Gly Met Lys Glu Asp Gln Lys Gln Asn Glu
 305 310 315

cct ttt gtg gcc acc cag tca tct gcc tgc gtg gat ggc cct gca aac 1187
 Pro Phe Val Ala Thr Gln Ser Ser Ala Cys Val Asp Gly Pro Ala Asn
 320 325 330 335

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 35 40 45

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 50 55 60

Glu Glu His Glu Cys Leu Ser Glu Gln Gln Leu Glu Gln Phe Leu Gly
 65 70 75 80

Arg Val Leu Glu Ala Ser Asn Tyr Gly Val Ser Val Leu Ser Asn Ala
85 90 95

Ser Gly Asn Trp Asn Trp Asp Phe Thr Ser Ala Leu Phe Phe Ala Ser
100 105 110

Thr Val Leu Ser Thr Thr Gly Tyr Gly His Thr Val Pro Leu Ser Asp
115 120 125

Gly Gly Lys Ala Phe Cys Ile Ile Tyr Ser Val Ile Gly Ile Pro Phe
130 135 140

Thr Leu Leu Phe Leu Thr Ala Val Val Gln Arg Ile Thr Val His Val
145 150 155 160

Thr Arg Arg Pro Val Leu Tyr Phe His Ile Arg Trp Gly Phe Ser Lys
165 170 175

Gln Val Val Ala Ile Val His Ala Val Leu Leu Gly Phe Val Thr Val
180 185 190

Ser Cys Phe Phe Phe Ile Pro Ala Ala Val Phe Ser Val Leu Glu Asp
195 200 205

Asp Trp Asn Phe Leu Glu Ser Phe Tyr Phe Cys Phe Ile Ser Leu Ser
210 215 220

Thr Ile Gly Leu Gly Asp Tyr Val Pro Gly Glu Gly Tyr Asn Gln Lys
225 230 235 240

Phe Arg Glu Leu Tyr Lys Ile Gly Ile Thr Cys Tyr Leu Leu Gly
245 250 255

Leu Ile Ala Met Leu Val Val Leu Glu Thr Phe Cys Glu Leu His Glu
260 265 270

Leu Lys Lys Phe Arg Lys Met Phe Tyr Val Lys Lys Asp Lys Asp Glu
275 280 285

Asp Gln Val His Ile Ile Glu His Asp Gln Leu Ser Phe Ser Ser Ile
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Thr Asp Gln Ala Ala Gly Met Lys Glu Asp Gln Lys Gln Asn Glu Pro
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<222> (126)..(1307)

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 1 5 10 15
 ttc acc tac ctg ctg gtg ggc gcc gtc ttc gac gcg ctg gag tcg 218
 Phe Thr Tyr Leu Leu Val Gly Ala Ala Val Phe Asp Ala Leu Glu Ser
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 gag ccc gag ctg atc gag cgg cag cgg ctg gag ctg cgg cag cag gag 266
 Glu Pro Glu Leu Ile Glu Arg Gln Arg Leu Glu Leu Arg Gln Gln Glu
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 ctg cgg cgc tac aac ctc agc cag ggc ggc tac gag gag ctg gag 314
 Leu Arg Ala Arg Tyr Asn Leu Ser Gln Gly Gly Tyr Glu Glu Leu Glu
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 Arg Val Val Leu Arg Leu Lys Pro His Lys Ala Gly Val Gln Trp Arg
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 Phe Ala Gly Ser Phe Tyr Phe Ala Ile Thr Val Ile Thr Thr Ile Gly
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 tac tgc ttc atc acc ctc acc acc atc ggc ttc ggc gac tac gtg gcg 746
 Tyr Cys Phe Ile Thr Leu Thr Ile Gly Phe Gly Asp Tyr Val Ala
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 ctg cag aag gac cag gcc ctg cag acg cag ccg cag tac gtg gcc ttc 794
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agc ttc gtc tac atc ctt acg ggc ctc acg gtc atc ggc gcc ttc ctc 842
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 Gly Gly Gly Gly Gly Ser Ala His Thr Thr Asp Thr Ala Ser Ser
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Phe Arg Gly Leu Met Lys Arg Arg Ser Ser Val
385 390

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385 390

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Arg Ala Arg Tyr Asn Leu Ser Gln Gly Gly Tyr Glu Glu Leu Glu Arg
50 55 60
Val Val Leu Arg Leu Lys Pro His Lys Ala Gly Val Gln Trp Arg Phe
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Ala Gly Ser Phe Tyr Phe Ala Ile Thr Val Ile Thr Thr Ile Gly Tyr
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Gly His Ala Ala Pro Ser Thr Asp Gly Gly Lys Val Phe Cys Met Phe
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Tyr Ala Leu Leu Gly Ile Pro Leu Thr Leu Val Met Phe Gln Ser Leu
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Gly Glu Arg Ile Asn Thr Leu Val Arg Tyr Leu Leu His Arg Ala Lys
130 135 140
Lys Gly Leu Gly Met Arg Arg Ala Asp Val Ser Met Ala Asn Met Val

145 150 155 160
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165 170 175
Ala Phe Ser His Tyr Glu His Trp Thr Phe Phe Gln Ala Tyr Tyr Tyr
180 185 190
Cys Phe Ile Thr Leu Thr Thr Ile Gly Phe Gly Asp Tyr Val Ala Leu
195 200 205
Gln Lys Asp Gln Ala Leu Gln Thr Gln Pro Gln Tyr Val Ala Phe Ser
210 215 220
Phe Val Tyr Ile Leu Thr Gly Leu Thr Val Ile Gly Ala Phe Leu Asn
225 230 240
Leu Val Val Leu Arg Phe Met Thr Met Asn Ala Glu Asp Glu Lys Arg
245 250 255
Asp Ala Glu His Arg Ala Leu Leu Thr Arg Asn Gly Gln Ala Gly Gly
260 265 270
Gly Gly Gly Gly Ser Ala His Thr Thr Asp Thr Ala Ser Ser Thr
275 280 285
Ala Ala Ala Gly Gly Gly Phe Arg Asn Val Tyr Ala Glu Val Leu
290 295 300
His Phe Gln Ser Met Cys Ser Cys Leu Trp Tyr Lys Ser Arg Glu Lys
305 310 320
Leu Gln Tyr Ser Ile Pro Met Ile Ile Pro Arg Asp Leu Ser Thr Ser
325 330 335
Asp Thr Cys Val Glu Gln Ser His Ser Ser Pro Gly Gly Gly Arg
340 345 350
Tyr Ser Asp Thr Pro Ser Arg Arg Cys Leu Cys Ser Gly Ala Pro Arg
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Ser Ala Ile Ser Ser Val Ser Thr Gly Leu His Ser Leu Ser Thr Phe
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Arg Gly Leu Met Lys Arg Arg Ser Ser Val
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Tyr Asn Leu Ser Glu Gly Gly Tyr Glu Glu Leu Glu Arg Val Val Leu
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Arg Leu Lys Pro His Lys Ala Gly Val Gln Trp Arg Phe Ala Gly Ser
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Phe Tyr Phe Ala Ile Thr Val Ile Thr Thr Ile Gly Tyr Gly His Ala
 85 90 95

Ala Pro Ser Thr Asp Gly Gly Lys Val Phe Cys Met Phe Tyr Ala Leu
 100 105 110

Leu Gly Ile Pro Leu Thr Leu Ile Met Phe Gln Ser Leu Gly Glu Arg
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Ile Asn Thr Phe Val Arg Tyr Leu Leu His Arg Ala Lys Arg Gly Leu
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Gly Met Arg His Ala Glu Val Ser Met Ala Asn Met Val Leu Ile Gly
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Phe Val Ser Cys Ile Ser Thr Leu Cys Ile Gly Ala Ala Ala Phe Ser
 165 170 175

Tyr Tyr Glu Arg Trp Thr Phe Phe Gln Ala Tyr Tyr Tyr Cys Phe Ile
 180 185 190

Thr Leu Thr Thr Ile Gly Phe Gly Asp Tyr Val Ala Leu Gln Lys Asp
 195 200 205

Gln Ala Leu Gln Thr Gln Pro Gln Tyr Val Ala Phe Ser Phe Val Tyr
 210 215 220

Ile Leu Thr Gly Leu Thr Val Ile Gly Ala Phe Leu Asn Leu Val Val
 225 230 235 240

Leu Arg Phe Met Thr Met Asn Ala Glu Asp Glu Lys Arg Asp Ala Glu
 245 250 255

His Arg Ala Leu Leu Thr His Asn Gly Gln Ala Val Gly Leu Gly Gly
 260 265 270

Leu Ser Cys Leu Ser Gly Ser Leu Gly Asp Val Arg Pro Arg Asp Pro
 275 280 285

Val Thr Cys Ala Ala Ala Gly Gly Val Gly Val Gly Val Gly Gly
 290 295 300

Ser Gly Phe Arg Asn Val Tyr Ala Glu Val Leu His Phe Gln Ser Met
 305 310 315 320

Cys Ser Cys Leu Trp Tyr Lys Ser Arg Glu Lys Leu Gln Tyr Ser Ile
 325 330 335

Pro Met Ile Ile Pro Arg Asp Leu Ser Thr Ser Asp Thr Cys Val Glu
 340 345 350

His Ser His Ser Ser Pro Gly Gly Gly Arg Tyr Ser Asp Thr Pro
355 360 365
Ser His Pro Cys Leu Cys Ser Gly Thr Gln Arg Ser Ala Ile Ser Ser
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Val Ser Thr Gly Leu His Ser Leu Ala Ala Phe Arg Gly Leu Met Lys
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Arg Arg Ser Ser Val
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35 40 45
Phe Asn Leu Ile Gly Ala Gly Ile Phe Tyr Leu Ala Glu Thr Gln Asn
50 55 60
Ser Ser Glu Ser Leu Asn Glu Asn Ser Glu Val Ser Lys Cys Leu His
65 70 75 80
Asn Leu Pro Ile Gly Gly Lys Ile Thr Ala Glu Met Lys Ser Lys Leu
85 90 95
Gly Lys Cys Leu Thr Lys Ser Ser Arg Ile Asp Gly Phe Gly Lys Ala
100 105 110
Ile Phe Phe Ser Trp Thr Leu Tyr Ser Thr Val Gly Tyr Gly Ser Leu
115 120 125
Tyr Pro His Ser Thr Leu Gly Arg Tyr Leu Thr Ile Phe Tyr Ser Leu
130 135 140
Leu Met Ile Pro Val Phe Ile Ala Phe Lys Phe Glu Phe Gly Thr Phe
145 150 155 160
Leu Ala His Phe Leu Val Val Ser Asn Arg Thr Arg Leu Ala Val
165 170 175
Lys Lys Ala Tyr Tyr Lys Leu Ser Gln Asn Pro Glu Asn Ala Glu Thr
180 185 190
Pro Ser Asn Ser Leu Gln His Asp Tyr Leu Ile Phe Leu Ser Ser Leu
195 200 205

Leu Leu Cys Ser Ile Ser Leu Leu Ser Ser Ser Ala Leu Phe Ser Ser
210 215 220
Ile Glu Asn Ile Ser Tyr Leu Ser Ser Val Tyr Phe Gly Ile Ile Thr
225 230 235 240
Met Phe Leu Ile Gly Ile Gly Asp Ile Val Pro Thr Asn Leu Val Trp
245 250 255
Phe Ser Gly Tyr Cys Met Leu Phe Leu Ile Ser Asp Val Leu Ser Asn
260 265 270
Gln Ile Phe Tyr Phe Cys Gln Ala Arg Val Arg Tyr Phe Phe His Ile
275 280 285
Leu Ala Arg Lys Ile Leu Leu Arg Glu Glu Asp Asp Gly Phe Gln
290 295 300
Leu Glu Thr Thr Val Ser Leu Gln His Ile Pro Ile Ile Asn Ser Gln
305 310 315 320
Cys Met Pro Ser Leu Val Leu Asp Cys Glu Lys Glu Glu Leu Asp Asn
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Asp Glu Lys Leu Ile Ser Ser Leu Thr Ser Thr
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35 40 45
Val Thr Tyr Ala Leu Gly Gly Ala Tyr Leu Phe Leu Ser Ile Glu His
50 55 60
Pro Glu Glu Leu Lys Arg Arg Glu Lys Ala Ile Arg Glu Phe Gln Asp
65 70 75 80
Leu Lys Gln Gln Phe Met Gly Asn Ile Thr Ser Gly Ile Glu Asn Ser
85 90 95
Glu Gln Ser Ile Glu Ile Tyr Thr Lys Lys Leu Ile Leu Met Leu Glu
100 105 110
Asp Ala His Asn Ala His Ala Phe Glu Tyr Phe Phe Leu Asn His Glu
115 120 125

Ile Pro Lys Asp Met Trp Thr Phe Ser Ser Ala Leu Val Phe Thr Thr
130 135 140

Thr Thr Val Ile Pro Val Gly Tyr Gly Tyr Ile Phe Pro Val Ser Ala
145 150 155 160

Tyr Gly Arg Met Cys Leu Ile Ala Tyr Ala Leu Leu Gly Ile Pro Leu
165 170 175

Thr Leu Val Thr Met Ala Asp Thr Gly Lys Phe Ala Ala Gln Leu Val
180 185 190

Thr Arg Trp Phe Gly Asp Asn Asn Met Ala Ile Pro Ala Ala Ile Phe
195 200 205

Val Cys Leu Leu Phe Ala Tyr Pro Leu Val Val Gly Phe Ile Leu Cys
210 215 220

Ser Thr Ser Asn Ile Thr Tyr Leu Asp Ser Val Tyr Phe Ser Leu Thr
225 230 235 240

Ser Ile Phe Thr Ile Gly Phe Gly Asp Leu Thr Pro Asp Met Asn Val
245 250 255

Ile His Met Val Leu Phe Leu Ala Val Gly Val Ile Leu Val Thr Ile
260 265 270

Thr Leu Asp Ile Val Ala Ala Glu Met Ile Asp Arg Val His Tyr Met
275 280 285

Gly Arg His Val Gly Lys Ala Lys Glu Leu Ala Gly Lys Met Phe Gln
290 295 300

Leu Ala Gln Ser Leu Asn Met Lys Gln Gly Leu Val Ser Gly Val Gly
305 310 315 320

Gln Leu His Ala Leu Ala Arg Phe Gly Met Leu Val Gly Arg Glu Glu
325 330 335

Val Asp Lys Thr Gln Glu Asp Gly Ile Ile Ala Phe Ser Pro Asp Val
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Met Asp Gly Leu Glu Phe Met Asp Thr Leu Ser Ile Tyr Ser Arg Arg
355 360 365

Ser Arg Arg Ser Ala Glu Asn Ser Ala Arg Asn Leu Phe Leu Ser
370 375 380

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<211> 370
<212> PRT
<213> Murine

<220>
<223> TREK-1

<400> 8
Met Ala Ala Pro Asp Leu Leu Asp Pro Lys Ser Ala Ala Gln Asn Ser
1 5 10 15

Lys Pro Arg Leu Ser Phe Ser Ser Lys Pro Thr Val Leu Ala Ser Arg
20 25 30

Val Glu Ser Asp Ser Ala Ile Asn Val Met Lys Trp Lys Thr Val Ser
35 40 45

Thr Ile Phe Leu Val Val Leu Tyr Leu Ile Ile Gly Ala Ala Val
50 55 60

Phe Lys Ala Leu Glu Gln Pro Gln Glu Ile Ser Gln Arg Thr Thr Ile
65 70 75 80

Val Ile Gln Lys Gln Thr Phe Ile Ala Gln His Ala Cys Val Asn Ser
85 90 95

Thr Glu Leu Asp Glu Leu Ile Gln Gln Ile Val Ala Ala Ile Asn Ala
100 105 110

Gly Ile Ile Pro Leu Gly Asn Ser Ser Asn Gln Val Ser His Trp Asp
115 120 125

Leu Gly Ser Ser Phe Phe Ala Gly Thr Val Ile Thr Thr Ile Gly
130 135 140

Phe Gly Asn Ile Ser Pro Arg Thr Glu Gly Gly Lys Ile Phe Cys Ile
145 150 155 160

Ile Tyr Ala Leu Leu Gly Ile Pro Leu Glu Gly Phe Leu Leu Ala Gly
165 170 175

Val Gly Asp Gln Leu Gly Thr Ile Phe Gly Lys Gly Ile Ala Lys Val
180 185 190

Glu Asp Thr Phe Ile Lys Trp Asn Val Ser Gln Thr Lys Ile Arg Ile
195 200 205

Ile Ser Thr Ile Ile Phe Ile Leu Phe Gly Cys Val Leu Phe Val Ala
210 215 220

Leu Pro Ala Val Ile Phe Lys His Ile Glu Gly Trp Ser Ala Leu Asp
225 230 235 240

Ala Ile Tyr Phe Val Val Ile Thr Leu Thr Thr Ile Gly Phe Gly Asp
245 250 255

Tyr Val Ala Gly Gly Ser Asp Ile Glu Tyr Leu Asp Phe Tyr Lys Pro
260 265 270

Val Val Trp Phe Trp Ile Leu Val Gly Leu Ala Tyr Phe Ala Ala Val
275 280 285

Leu Ser Met Ile Gly Asp Trp Leu Arg Val Ile Ser Lys Lys Thr Lys
290 295 300

Glu Glu Val Gly Glu Phe Arg Ala His Ala Ala Glu Trp Thr Ala Asn
305 310 315 320

Val Thr Ala Glu Phe Lys Glu Thr Arg Arg Arg Leu Ser Val Glu Ile
325 330 335

Tyr Asp Lys Phe Gln Arg Ala Thr Ser Val Lys Arg Lys Leu Ser Ala
340 345 350

Glu Leu Ala Gly Asn His Asn Gln Glu Leu Thr Pro Cys Met Arg Thr
355 360 365

Cys Leu
370

<210> 9
<211> 27
<212> PRT
<213> Homo sapiens

<220>
<223> TWIK-1 P1

<400> 9
Phe Thr Ser Ala Leu Phe Phe Ala Ser Thr Val Leu Ser Thr Thr Gly
1 5 10 15

Tyr Gly His Thr Val Pro Leu Ser Asp Gly Gly
20 25

<210> 10
<211> 27
<212> PRT
<213> Homo sapiens

<220>
<223> TWIK-1 P2

<400> 10
Phe Leu Glu Ser Phe Tyr Phe Cys Phe Ile Ser Leu Ser Thr Ile Gly
1 5 10 15

Leu Gly Asp Tyr Val Pro Gly Glu Gly Tyr Asn
20 25

<210> 11
<211> 27
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism: P domain of
representative K+ channel sequence

<220>
<223> TOK-1 P2

<400> 11
Tyr Phe Asn Cys Ile Tyr Phe Cys Phe Leu Cys Leu Leu Thr Ile Gly
1 5 10 15

Tyr Gly Asp Tyr Ala Pro Arg Thr Gly Ala Gly
20 25

<210> 12
<211> 27
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism: P domain of representative K⁺ channel sequence

<220>
<223> TOK-1 P1

<400> 12
Tyr Gly Asn Ala Leu Tyr Phe Cys Thr Val Ser Leu Leu Thr Val Gly
1 5 10 15

Leu Gly Asp Ile Leu Pro Lys Ser Val Gly Ala
20 25

<210> 13
<211> 27
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism: P domain of representative K⁺ channel sequence

<220>
<223> Slo

<400> 13
Tyr Trp Thr Cys Val Tyr Phe Leu Ile Val Thr Met Ser Thr Val Gly
1 5 10 15

Tyr Gly Asp Val Tyr Cys Glu Thr Val Leu Gly
20 25

<210> 14
<211> 27
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism: P domain of representative K⁺ channel sequence

<220>
<223> Shaker

<400> 14
Ile Pro Asp Ala Phe Trp Trp Ala Val Val Thr Met Thr Thr Val Gly
1 5 10 15

Tyr Gly Asp Met Thr Pro Val Gly Phe Trp Gly
20 25

<210> 15
<211> 27
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism: P domain of
representative K⁺ channel sequence

<220>
<223> Shab

<400> 15
Ile Pro Glu Ala Phe Trp Trp Ala Gly Ile Thr Met Thr Thr Val Gly
1 5 10 15

Tyr Gly Asp Ile Cys Pro Thr Thr Ala Leu Gly
20 25

<210> 16
<211> 27
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism: P domain of
representative K⁺ channel sequence

<220>
<223> Shal

<400> 16
Ile Pro Ala Ala Phe Trp Tyr Thr Ile Val Thr Met Thr Thr Leu Gly
1 5 10 15

Tyr Gly Asp Met Val Pro Glu Thr Ile Ala Gly
20 25

<210> 17
<211> 27
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism: P domain of
representative K⁺ channel sequence

<220>
<223> Shaw

<400> 17
Ile Pro Leu Gly Leu Trp Trp Ala Leu Val Thr Met Thr Thr Val Gly
1 5 10 15

Tyr Gly Asp Met Ala Pro Lys Thr Tyr Ile Gly
20 25

<210> 18

<211> 27
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism: P domain of representative K+ channel sequence

<220>
<223> KAT1

<400> 18
Tyr Val Thr Ala Leu Tyr Trp Ser Ile Thr Thr Leu Thr Thr Gly
1 5 10 15

Tyr Gly Asp Phe His Ala Glu Asn Pro Arg Glu
20 25

16 15 14 13 12 11 10 9 8 7 6 5 4 3 2 1

<210> 19
<211> 27
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism: P domain of representative K+ channel sequence

<220>
<223> AKT1

<400> 19
Tyr Val Thr Ser Met Tyr Trp Ser Ile Thr Thr Leu Thr Thr Val Gly
1 5 10 15

Tyr Gly Asp Ile His Pro Val Asn Thr Lys Glu
20 25

16 15 14 13 12 11 10 9 8 7 6 5 4 3 2 1

<210> 20
<211> 27
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism: P domain of representative K+ channel sequence

<220>
<223> eag

<400> 20
Tyr Val Thr Ala Leu Tyr Phe Thr Met Thr Cys Met Thr Ser Val Gly
1 5 10 15

Phe Gly Asn Val Ala Ala Glu Thr Asp Asn Glu
20 25

16 15 14 13 12 11 10 9 8 7 6 5 4 3 2 1

<210> 21
<211> 27

<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism: P domain of
representative K⁺ channel sequence

<220>
<223> ROMK1

<400> 21
Met Thr Ser Ala Phe Leu Phe Ser Leu Glu Thr Gln Val Thr Ile Gly
1 5 10 15
Tyr Gly Phe Arg Phe Val Thr Glu Gln Cys Ala
20 25

TOP60
<210> 22
<211> 27
<212> PRT
<213> Unknown

TOP60
<220>
<223> Description of Unknown Organism: P domain of
representative K⁺ channel sequence

TOP60
<220>
<223> IRK1

TOP60
<400> 22
Phe Thr Ala Ala Phe Leu Phe Ser Ile Glu Thr Gln Thr Thr Ile Gly
1 5 10 15
Tyr Gly Phe Arg Cys Val Thr Asp Glu Cys Pro
20 25

TOP60
<210> 23
<211> 27
<212> PRT
<213> Unknown

TOP60
<220>
<223> Description of Unknown Organism: P domain of
representative K⁺ channel sequence

TOP60
<220>
<223> GIRK1

TOP60
<400> 23
Phe Pro Ser Ala Phe Leu Phe Phe Ile Glu Thr Glu Ala Thr Ile Gly
1 5 10 15
Tyr Gly Tyr Arg Tyr Ile Thr Asp Lys Cys Pro
20 25

TOP60
<210> 24
<211> 48
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: antisense
oligonucleotide complementary to the partial
mouse cDNA sequence of TASK

<400> 24

caccagcagg taggtgaagg tgcacacgat gagagccaac gtgcgcac

48